

1/5

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GmmoriAe ..... CTACGG GTAACATCTT TATTAGTTAT
GmmoriAc .....GCT TTGTCTACGG GTAACATCTT TATTAGTTAT

GmmoriAe CGTAAATAA CAGATTGTAG AAATGAAGTT TACAGGAATA TTCTTCATAA
GmmoriAc CGTAAATAA CAGATTGTAG AAATGAATT TACAGGAATA TTCTTCATGA

GmmoriAe TTATGGCGAT CATTGCCCTC TTTATAGGGT CAAATGAAGC GCGCGCTAAA
GmmoriAc TTATGGCGAT CATTGCCCTC TTTATAGGGT CAAATGAAGC GCGCGCTAAA

GmmoriAe GTCAATGTTA ATGCCATTAA GAAGGGAGGA AAGGCCATAG GAAAAGGATT
GmmoriAc GTCAATGTTA ATGCCATTAA GAAGGGAGGA AAGGCCATAG GAAAAGGATT

GmmoriAe TAAAGTAATC AGTGC GCGCA GTACAGCGCA TGACGTCTAT GAACACATTA
GmmoriAc TAAAGTAATC AGTGC GCGCA GTACAGCGCA TGACGTCTAT GAACACATTA

GmmoriAe AAAACAGAAG GCACTAATAA AACCAAAAAT AATTATTTAT TTTATAAGGT
GmmoriAc AAAACAGAAG GCACTAATAG AACCAAAAAT AATCATTAT TTTATAAGGT

GmmoriAe AATTTTAAGA CATATAATGT ATGTTGCAAA TTATTAAGTG AAATAAAATA
GmmoriAc AATTTTAAGA CATATAATGA ATGTTGCAAA TTATTAAGTG GAATAAAATA

GmmoriAe TAAAATATTT TTTGTT
GmmoriAc TAAAATATTT TTTGTT

```

Figure 1

	1		50
GmmoriAe	MKFTGIFFII	MAIIALFIGS	NEAAPKVVVN AIKKGGAIG KGFKVISAAS
GmmoriAc	MNFTGIFFMI	MAIIALFIGS	NEAAPKVVVN AIKKGGAIG KGFKVISAAS
	51	64	
GmmoriAe	TAHDVYEHK	NRRH*	
GmmoriAc	TAHDVYEHK	NRRH*	

Figure 2

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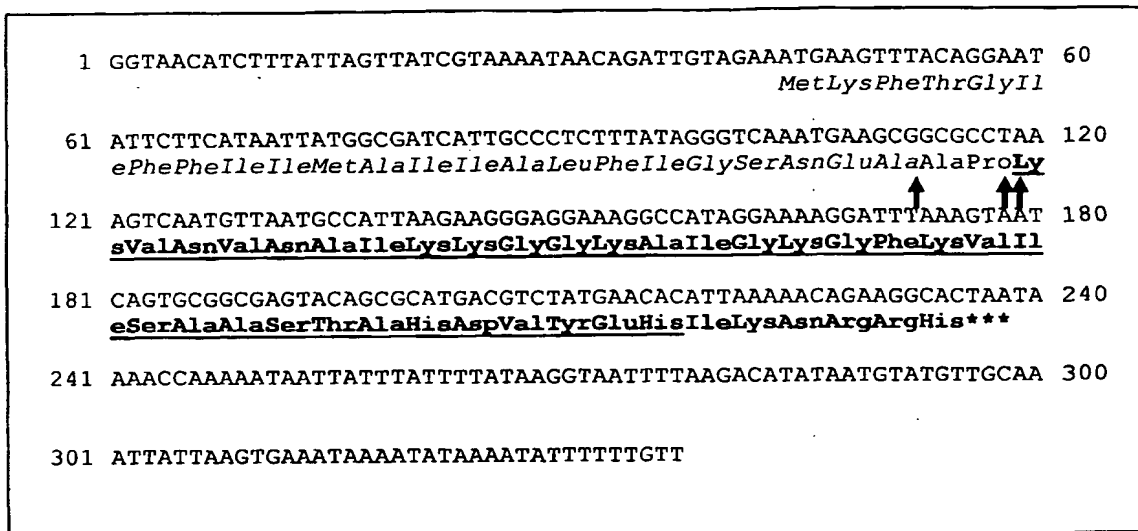


Figure 3

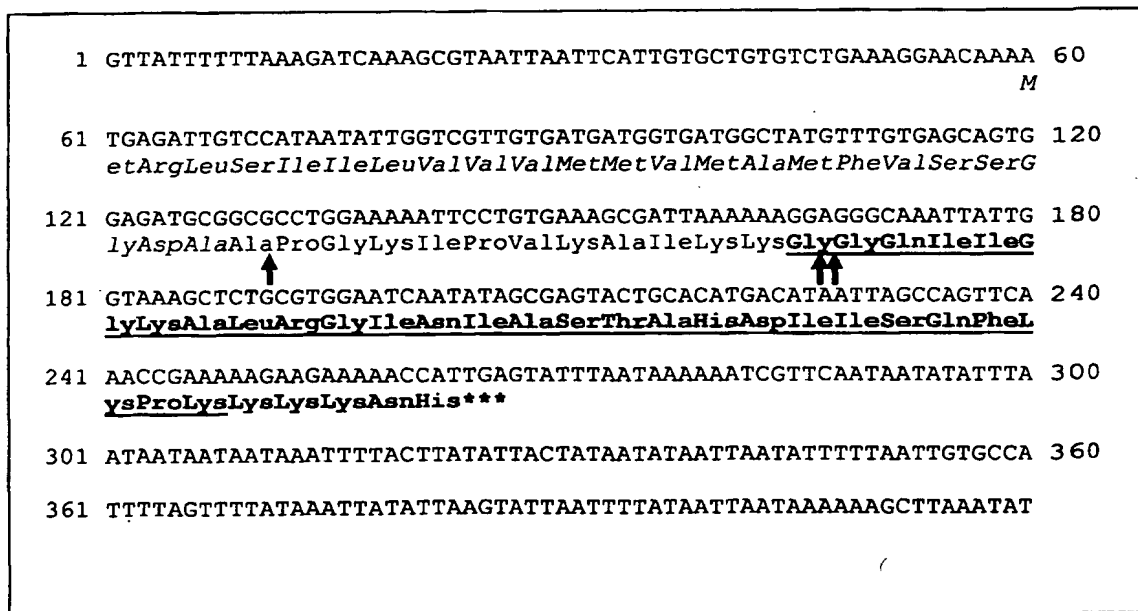


Figure 4

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1 GTAACAGTACCACCGGTGTACAGTCGCAGTAGTTAGTCTTCAATCTTAGTGAAAACCTTCGG

61 TTCTCTTTATCAACCATGAAGCTGACCGGCTCATTATTTTCATGATCATGGCGATGCTCGCC
 MetLysLeuThrGlyLeuPhePheMetIleMetAlaMetLeuAla
 Val

121 CTGTTTGTTGGCGCTGGTCAAGCCGACCCTAAGGTGCCCATTTGGCGCCATCAAGAAGGGT
 LeuPheValGlyAlaGlyGlnAlaAspProLysValProIleGlyAlaIleLysLysGly

 ↑ ↑↑

181 GGCAA~~A~~AATTATAAAAAAGGTCTTGGTGTAATTGGTGCCGCTGGTACAGCGCATGAAGTA
GlyLysIleIleLysLysGlyLeuGlyValIleGlyAlaAlaGlyThrAlaHisGluVal

241 TATAGCCACGTCAAGAACAGGCATTAGATTCTTGAAGAATATATAGTATATAATTATGAA
TyrSerHisValLysAsnArgHis***

301 GTACTATCCTTTTGTATATGTGACTAAGTGCATAATGTAAAGTCAAATGAAATATATATT

361 ATTTATCCTCGTGCC

Figure 5

1 ACTTCATTGTGTACAGTTGCAGGACTTAATACTTAGTGAAC TACTTACTCCTCGTTACCA

61 ACCATGAAGCTGACCGGTCTATTTCTCATGATCATGGCGGTGCTCGCGCTGTTTGTGTC
MetLysLeuThrGlyLeuPheLeuMetIleMetAlaValLeuAlaLeuPheValGly

121 GCTGGTCAAGCCGACCTAAGGTGCCCATTTGGCGCTATCAAGAAGGGCGGCAAAATTATT
AlaGlyGlnAlaAspProLysValProIleGlyAlaIleLysLysGlyGlyLysIleIle

181 AAAAAGGGTCTAGGTGTGCTTGGCGCCGCGGGCAGCGCACGAAGTGTACAACCACGTT
LysLysGlyLeuGlyValLeuGlyAlaAlaGlyThrAlaHisGluValTyrAsnHisVal

241 AGGAACAGGCAGTAACGTCATGCGTGATTGTTGTACATACAGTACTTACAATACGATTTG
ArgAsnArgGln***

301 TCTTGGCTGTGATATATCTTTAGATAAATTAATTTATAATACCACATACTTATTAGTAAA

361 ATACTCAAATATATTGATTATAGATACATTAATAAAATATTAATTATTACAATATTTTGT

421 TTTATGTACAATGCGAATAGATTCTACCCTCTGCCTCGTGCC

Figure 6

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GmmoriC1 GTAACAGTACCACCGTGTACAGTCGCAGTAGTTAGTCTTCAATCTTAGTGAAAACCTTCGC 60
 GmmoriC2ACTTCATTGTGTACAGTTGCAGGACTTAATA.....CTTAGTGAACTACTTAC 48

GmmoriC1 TTCTCTTTATCAACCATGAAGCTGACCGGTCTATTTTTCATGATCATGGCGATGCTCGCC 120
 GmmoriC2 TCCTCGTTACCAACCATGAAGCTGACCGGTCTATTTCTCATGATCATGGCGGTGCTCGCG 108

GmmoriC1 CTGTTTGTGGCGCTGGTCAAGCCGACCCTAAGGTGCCCATTGGCGCCATCAAGAAGGGT 180
 GmmoriC2 CTGTTTGTGGCGCTGGTCAAGCCGACCCTAAGGTGCCCATTGGCGCTATCAAGAAGGGC 168

GmmoriC1 GGCAAAATTATTAATAAAGGTCTTGGTGAATTGGTGCCGCTGGTACAGCGCATGAAGTA 240
 GmmoriC2 GGCAAAATTATTAATAAAGGTCTAGGTGTCTTGGCGCCGCGGGCACAGCGCACGAAGTG 228

GmmoriC1 TATAGCCACGTCAAGAACAGGCATTAGATTCTTGAAGAATATATAGTATATA.ATTA..T 297
 GmmoriC2 TACAACCACGTTAGGAACAGGCAGTAACGTCATGCGTGAT.TGTTGTACATACAGTACTT 287

GmmoriC1 GAAGTACTATCC.TTTTGTATATGTGAC.TAAGTGCATAATGTAAAGTCAAATGAAATAT 355
 GmmoriC2 ACAATACGATTTGTCTTGGCTGTGATATATCTTTAGATAAATTAATTTATAATACCACAT 347

GmmoriC1 A..TATTATTTA..TCCTCGTGCC 375
 GmmoriC2 ACTTATTAGTAAATACTCAAATA..... 462

Figure 7

GmmoriC1 MKLTGLFFMIMAMLALFVGAGQADPKVPIGAIKKGGKIIKKGLGVIGAAG
 GmmoriC2 MKLTGLFLMIMAVLALFVGAGQADPKVPIGAIKKGGKIIKKGLGVLGAAG

GmmoriC1 TAHEVYSHVKNRH
 GmmoriC2 TAHEVYNHVRNRQ

Figure 8

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Bmmor  MNILKFFFVFIVAMSLVSCS-TAAPAKIPIKAIKTVGKAVGKGLRAINIASTANDVFNFLKPKKRRKH-
Hpmor  -----AMSLVSCS-TAAPAKIPIKAIKTVGKAVGKGLRAINIASTANDVFNFLKPKKRRKH-
Hvvir  -----GKIPIGAIKKAGKAIGKGLRAVNIASTAHDVYTFKPKKR-H-
Slmor  MKLTKVFVILIVVVALLVPS-EAAPGKIPVKAIKKAGAAIGKGLRAINIASTAHDVYSFFKPKHKKKH
Semor  MKLTKVFVIVIVVVALLVPS-EAAPGKIPVKAIKKAGTAIGKGLRAINIASTAHDVYSFFKPKHKKKH
Msmor  MKLTSLFIFVIVALSLLFSSTDAAPGKIPVKAIKQAGKVIKGLRAINIAAGTTTHDVVSFFRPKKKKH-
CiP1647 -----RKIPVEAIKKG---ASRAWRALDLASTAYDIASIFN--RKRE-
CiP1648 -----GKIPVEALKKGAKVAGRAWRALDLASTAYDIAHLFD--RKRN-
CiP1646 -----GKIPINAIKKGAKAVGHGLRALNIASTAHDIASAFH--RKRKH
GmmoriB MRLSIILVVMMVMAMFVSSGDAAPGKIPVKAIKKGGQIIGKALRGINIASTAHDIISQFKPKKKKNH
GmmoriC1 MKLTGLFFMIMAMLALFVGAGQADP-KVPIGAIKKGGKI IKKGLGVIGAAGTAHEVYSHVKNRH----
GmmoriC2 MKLTGLFLMIMAVLALFVGAGQADP-KVPIGAIKKGGKI IKKGLGVIGAAGTAHEVYNHVRNRQ----
BmmorX  MYFLKYFIVVLVALSLMICSGQADP-KIPVKSLLKGGKVIAGFKVLTAAGTAHEVYSHVRNRGNQG-
Gmmoria MKFTGIFFIIMAIILFIGSNEAAP-KVNVNAIKKGGKAIGKGFKVISAASTAHDVYEHKNNRH---

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Figure 9